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RAW SEQUENCE LISTING   DATE: 02/15/2002
PATENT APPLICATION: US/10/056,794   TIME: 14:53:41

Input Set : A:\527c2.app
Output Set: N:\CRF3\02152002\J056794.raw

SEQUENCE LISTING
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 4 (1) GENERAL INFORMATION:
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C--> 6   (i) APPLICANT: Graves, Scott S.
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 7                        Reno, John M.
 8                        Mallett, Robert W.
 9                        Hylarides, Mark D.
10                        Searle, Stephen M.J.
11                        Henry, Andrew H.
12                        Pedersen, Jan T.
13                        Rees, Anthony R.
15      (ii) TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT BIND TO THE
16                        ANTIGEN BOUND BY ANTIBODY NR-LU-13 AND THEIR USE IN
17                        PRETARGETING METHODS
19     (iii) NUMBER OF SEQUENCES: 19
21      (iv) CORRESPONDENCE ADDRESS:
22          (A) ADDRESSEE: Seed IP Law Group
23          (B) STREET: 701 Fifth Avenue, Suite 6300
24          (C) CITY: Seattle
25          (D) STATE: Washington
26          (E) COUNTRY: USA
27          (F) ZIP: 98104
29       (v) COMPUTER READABLE FORM:
30          (A) MEDIUM TYPE: Floppy disk
31          (B) COMPUTER: IBM PC compatible
32          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
33          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
35      (vi) CURRENT APPLICATION DATA:
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C--> 36   (A) APPLICATION NUMBER: US/10/056,794
C--> 37   (B) FILING DATE: 24-Jan-2002
```
38          (C) CLASSIFICATION:
40    (viii) ATTORNEY/AGENT INFORMATION:
41          (A) NAME: Sharkey Ph.D., Richard G.
42          (B) REGISTRATION NUMBER: 32,629
43          (C) REFERENCE/DOCKET NUMBER: 690022.527C2
45      (ix) TELECOMMUNICATION INFORMATION:
46          (A) TELEPHONE: (206) 622-4900
47          (B) TELEFAX: (206) 682-6031
50 (2) INFORMATION FOR SEQ ID NO: 1:
52       (i) SEQUENCE CHARACTERISTICS:
53          (A) LENGTH: 31 base pairs
54          (B) TYPE: nucleic acid
55          (C) STRANDEDNESS: single
56          (D) TOPOLOGY: linear
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```
62      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64 CCTGACGAAT TCGTTGACAT TGATTATTGA C                          31
66 (2) INFORMATION FOR SEQ ID NO: 2:
68      (i) SEQUENCE CHARACTERISTICS:
69          (A) LENGTH: 32 base pairs
70          (B) TYPE: nucleic acid
71          (C) STRANDEDNESS: single
72          (D) TOPOLOGY: linear
78      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
80 CCTGACGCGG CCGCTTCGAT AAGCCAGTAA GC                          32
82 (2) INFORMATION FOR SEQ ID NO: 3:
84      (i) SEQUENCE CHARACTERISTICS:
85          (A) LENGTH: 44 base pairs
86          (B) TYPE: nucleic acid
87          (C) STRANDEDNESS: single
88          (D) TOPOLOGY: linear
94      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
96 GTTCGGCTCG AGCACAGCTA GCATTATCTG GGATAAGCAT GCTG             44
98 (2) INFORMATION FOR SEQ ID NO: 4:
100     (i) SEQUENCE CHARACTERISTICS:
101         (A) LENGTH: 34 base pairs
102         (B) TYPE: nucleic acid
103         (C) STRANDEDNESS: single
104         (D) TOPOLOGY: linear
110     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
112 GTTACGGGGC CCCTAACACT CTCCCCTGTT GAAG                       34
114 (2) INFORMATION FOR SEQ ID NO: 5:
116     (i) SEQUENCE CHARACTERISTICS:
117         (A) LENGTH: 28 base pairs
118         (B) TYPE: nucleic acid
119         (C) STRANDEDNESS: single
120         (D) TOPOLOGY: linear
126     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
128 GTACGCGGAT CCCAGACACT GGACGCTG                              28
130 (2) INFORMATION FOR SEQ ID NO: 6:
132     (i) SEQUENCE CHARACTERISTICS:
133         (A) LENGTH: 30 base pairs
134         (B) TYPE: nucleic acid
135         (C) STRANDEDNESS: single
136         (D) TOPOLOGY: linear
142     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
144 CATTCGGAAT TCGAACCATC ACAGTCTCGC                            30
146 (2) INFORMATION FOR SEQ ID NO: 7:
148     (i) SEQUENCE CHARACTERISTICS:
149         (A) LENGTH: 34 base pairs
150         (B) TYPE: nucleic acid
151         (C) STRANDEDNESS: single
152         (D) TOPOLOGY: linear
158     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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160 GCTGACGAAT TCTCATTTAC CCGGAGACAG GGAG                          34
162 (2) INFORMATION FOR SEQ ID NO: 8:
164      (i) SEQUENCE CHARACTERISTICS:
165          (A) LENGTH: 26 base pairs
166          (B) TYPE: nucleic acid
167          (C) STRANDEDNESS: single
168          (D) TOPOLOGY: linear
174      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
176 CCGTCTATTA CTGTTCTAGA GAGGTC                                   26
178 (2) INFORMATION FOR SEQ ID NO: 9:
180      (i) SEQUENCE CHARACTERISTICS:
181          (A) LENGTH: 41 base pairs
182          (B) TYPE: nucleic acid
183          (C) STRANDEDNESS: single
184          (D) TOPOLOGY: linear
190      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
192 CAGCGTGCGG CCGCACCATG GACATCAGGG CTCCTGCTCA G                   41
194 (2) INFORMATION FOR SEQ ID NO: 10:
196      (i) SEQUENCE CHARACTERISTICS:
197          (A) LENGTH: 26 base pairs
198          (B) TYPE: nucleic acid
199          (C) STRANDEDNESS: single
200          (D) TOPOLOGY: linear
206      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
208 AGCAGTACCA AAGCACGTAC CGGGTG                                   26
210 (2) INFORMATION FOR SEQ ID NO: 11:
212      (i) SEQUENCE CHARACTERISTICS:
213          (A) LENGTH: 23 base pairs
214          (B) TYPE: nucleic acid
215          (C) STRANDEDNESS: single
216          (D) TOPOLOGY: linear
222      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
224 TACGTGCTTT GGTACTGCTC CTC                                      23
226 (2) INFORMATION FOR SEQ ID NO: 12:
228      (i) SEQUENCE CHARACTERISTICS:
229          (A) LENGTH: 34 base pairs
230          (B) TYPE: nucleic acid
231          (C) STRANDEDNESS: single
232          (D) TOPOLOGY: linear
238      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
240 GCTGACGGAT CCTCATTTAC CCGGAGACAG GGAG                          34
242 (2) INFORMATION FOR SEQ ID NO: 13:
244      (i) SEQUENCE CHARACTERISTICS:
245          (A) LENGTH: 26 base pairs
246          (B) TYPE: nucleic acid
247          (C) STRANDEDNESS: single
248          (D) TOPOLOGY: linear
254      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
256 CCGTCTATTA CTGTTCTAGA GAGGTC                                   26
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258 (2) INFORMATION FOR SEQ ID NO: 14:
260      (i) SEQUENCE CHARACTERISTICS:
261           (A) LENGTH: 360 base pairs
262           (B) TYPE: nucleic acid
263           (C) STRANDEDNESS: single
264           (D) TOPOLOGY: linear
268      (ix) FEATURE:
269           (A) NAME/KEY: CDS
270           (B) LOCATION: 1..360
273      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
275 GAG GTT CAG CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC         48
276 Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
277  1               5                   10                  15
279 TCA GTC AGG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC         96
280 Ser Val Arg Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
281              20                  25                  30
283 TAT ATG CAC TGG GTG ATA GAG AGG CCT GAA CAG GGC CTG GAG TGG ATT        144
284 Tyr Met His Trp Val Ile Glu Arg Pro Glu Gln Gly Leu Glu Trp Ile
285              35                  40                  45
287 GGA AGG ATT GAT CCT GCG AAT GGT AAT ACT AAA TGT GAC CCG AAG TTC        192
288 Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Cys Asp Pro Lys Phe
289      50                  55                  60
291 CAG GGC AAG GCC ACT ATA ACA GCA GAC ACA TCC TCC AAC ACA GCC TAC        240
292 Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
293  65                  70                  75                  80
295 CTG CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAT TAC TGT        288
296 Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
297              85                  90                  95
299 TCT AGA GAG GTC CTA ACT GGG ACG TGG TCT TTG GAC TAC TGG GGT CAA        336
300 Ser Arg Glu Val Leu Thr Gly Thr Trp Ser Leu Asp Tyr Trp Gly Gln
301              100                 105                 110
303 GGA ACC TCA GTC ACC GTC TCC TCA                                        360
304 Gly Thr Ser Val Thr Val Ser Ser
305              115                 120
308 (2) INFORMATION FOR SEQ ID NO: 15:
310      (i) SEQUENCE CHARACTERISTICS:
311           (A) LENGTH: 120 amino acids
312           (B) TYPE: amino acid
313           (D) TOPOLOGY: linear
315      (ii) MOLECULE TYPE: protein
317      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
319 Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
320  1               5                   10                  15
322 Ser Val Arg Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
323              20                  25                  30
325 Tyr Met His Trp Val Ile Glu Arg Pro Glu Gln Gly Leu Glu Trp Ile
326              35                  40                  45
328 Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Cys Asp Pro Lys Phe
329      50                  55                  60
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331 Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
332  65              70              75              80
334 Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
335              85              90              95
337 Ser Arg Glu Val Leu Thr Gly Thr Trp Ser Leu Asp Tyr Trp Gly Gln
338             100             105             110
340 Gly Thr Ser Val Thr Val Ser Ser
341         115             120
344 (2) INFORMATION FOR SEQ ID NO: 16:
346     (i) SEQUENCE CHARACTERISTICS:
347         (A) LENGTH: 321 base pairs
348         (B) TYPE: nucleic acid
349         (C) STRANDEDNESS: single
350         (D) TOPOLOGY: linear
354     (ix) FEATURE:
355         (A) NAME/KEY: CDS
356         (B) LOCATION: 1..321
359     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
361 GAC ATC CAG ATG ATT CAG TCT CCA TCG TCC ATG TTT GCC TCT CTG GGA       48
362 Asp Ile Gln Met Ile Gln Ser Pro Ser Ser Met Phe Ala Ser Leu Gly
363  1               5              10              15
365 GAC AGA GTC AGT CTC TCT TGT CGG GCT AGT CAG GGC ATT AGA GGT AAT       96
366 Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Gly Ile Arg Gly Asn
367             20              25              30
369 TTA GAC TGG TAT CAG CAG AAA CCA GGT GGA ACT ATT AAA CTC CTG ATC      144
370 Leu Asp Trp Tyr Gln Gln Lys Pro Gly Gly Thr Ile Lys Leu Leu Ile
371         35              40              45
373 TAC TCC ACA TCC AAT TTA AAT TCT GGT GTC CCA TCA AGG TTC AGT GGC      192
374 Tyr Ser Thr Ser Asn Leu Asn Ser Gly Val Pro Ser Arg Phe Ser Gly
375         50              55              60
377 AGT GGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC AGC CTA GAC TCT      240
378 Ser Gly Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Asp Ser
379  65              70              75              80
381 GAA GAT TTT GCA GAC TAT TAC TGT CTA CAG CGT AAT GCG TAT CCG TAC      288
382 Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Arg Asn Ala Tyr Pro Tyr
383             85              90              95
385 ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA                          321
386 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
387         100             105
390 (2) INFORMATION FOR SEQ ID NO: 17:
392     (i) SEQUENCE CHARACTERISTICS:
393         (A) LENGTH: 107 amino acids
394         (B) TYPE: amino acid
395         (D) TOPOLOGY: linear
397     (ii) MOLECULE TYPE: protein
399     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
401 Asp Ile Gln Met Ile Gln Ser Pro Ser Ser Met Phe Ala Ser Leu Gly
402  1               5              10              15
404 Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Gly Ile Arg Gly Asn
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VERIFICATION SUMMARY   DATE: 02/15/2002
PATENT APPLICATION: **US/10/056,794**   TIME: 14:53:42

Input Set : **A:\527c2.app**
Output Set: **N:\CRF3\02152002\J056794.raw**

L:6 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:36 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:37 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]